

Amendments to the Claims

Claim 1 (Currently amended): A method for genetically identifying the reproductive longevity potential of a pig comprising:
obtaining a sample of genetic material from a pig;
assaying for the presence of a polymorphism in the insulin-like growth factor 1 receptor gene (IGF-1R) corresponding to position 3832 of SEQ ID NO:23, wherein the polymorphism is a thymidine at position 3832 of SEQ ID NO: 23, the polymorphism being associated with reproductive longevity potential, wherein the trait of reproductive longevity potential is characterized by an increase in the number of pregnancies or the duration of time a pig is capable of reproduction relative to the mean of a given population, group or species; and
identifying that the pig has reproductive longevity potential if the pig has a thymidine at position 3832.

Claims 2-3 (Canceled).

Claim 4 (Original): The method of claim 1 wherein a step of assaying the polymorphism is selected from the group consisting of: direct sequencing, restriction fragment length polymorphism (RFLP) analysis, single-stranded conformation polymorphism (SSCP), PCR amplification of specific alleles, amplification of DNA target by PCR followed by a mini-sequencing assay, allelic discrimination during PCR, Genetic Bit Analysis, Pyrosequencing, oligonucleotide ligation assay, and analysis of melting curves.

Claim 5 (Original): The method of claim 4 wherein the step of assaying the polymorphism is RFLP.

Claim 6 (Original): The method of claim 4 wherein the step of assaying the polymorphism is SSCP.

Claim 7 (Previously presented): The method of claim 1 wherein the step of assaying for the presence of the polymorphism comprises the steps of:
digesting the genetic material with a restriction endonuclease that cleaves the gene in at least one place, wherein a particular restriction endonuclease pattern indicates the presence or absence of a polymorphism;
separating the fragments obtained from the digestion;
detecting a restriction pattern generated by the fragments; and
comparing the pattern with a second restriction pattern for the gene obtained by using the restriction endonuclease, wherein the second restriction pattern is associated with reproductive longevity potential.

Claim 8 (Original): The method of claim 7 wherein said separation is by gel electrophoresis.

Claim 9 (Original): The method of claim 7 further comprising:
amplifying the gene or a portion thereof which contains at least one polymorphism, prior to digestion.

Claim 10 (Original): The method of claim 9 wherein the amplification includes selecting a forward and a reverse sequence primer capable of amplifying a region of the gene which contains a polymorphism.

Claim 11 (Withdrawn): The method of claim 1 wherein the polymorphism is identified as an A to G nucleotide substitution at position 3876 of the gene.

Claim 12 (Withdrawn): The method of claim 1 wherein the polymorphism is identified as a G to A nucleotide substitution at position 331 of the gene.

Claim 13 (Withdrawn): The method of claim 1 wherein the polymorphism is a 12 base pair deletion at positions 3896-3907 of the gene.

Claim 14 (Withdrawn): The method of claim 7 wherein the restriction endonuclease is HpaII.

Claim 15 (Withdrawn): The method of claim 7 wherein the restriction endonuclease DpnII.

Claim 16 (Withdrawn): The method of claim 7 wherein the restriction endonuclease is TaqI.

Claim 17 (Withdrawn): The method of claim 7 wherein the restriction endonuclease is MnlI.

Claim 18 (Withdrawn): The method of claim 7 wherein the restriction endonuclease is AvaII.

Claim 19 (Withdrawn): The method of claim 10 wherein the forward primer is SEQ ID NO:8 and wherein the reverse primer is SEQ ID NO:9.

Claim 20 (Withdrawn): The method of claim 10 wherein the forward primer is SEQ ID NO:10 and wherein the reverse primer is SEQ ID NO:11.

Claim 21 (Withdrawn): The method of claim 10 wherein the forward primer is SEQ ID NO:12 and wherein the reverse primer is SEQ ID NO:13.

Claim 22 (Withdrawn): The method of claim 10 wherein the forward primer is SEQ ID NO:14 and wherein the reverse primer is SEQ ID NO:15.

Claim 23 (Withdrawn): The method of claim 10 wherein the forward primer is SEQ ID NO:16 and wherein the reverse primer is SEQ ID NO:17.

Claim 24 (Withdrawn): The method of claim 10 wherein the forward primer is SEQ ID NO:18 and wherein the reverse primer is SEQ ID NO:19.

Claim 25 (Currently amended): A method of screening pigs to determine those more likely to have reproductive longevity potential, the method comprising:

obtaining a biological sample from a pig ~~said pigs~~;

assaying for the presence of a ~~genotype in the~~ polymorphism in an IGF-1R gene corresponding to position 3832 of SEQ ID NO:23, ~~wherein the genotype is wherein said~~

polymorphism is a thymidine at position 3832 of SEQ ID NO: 23, said polymorphism being associated with reproductive longevity potential, wherein the trait of reproductive

longevity potential is characterized by an increase in the number of pregnancies or the duration of time a pig is capable of reproduction relative to the mean of a given

population, group or species, and characterized by a restriction fragment pattern, wherein said pattern when compared to a second restriction pattern is known to have or not have a

desired polymorphic marker, the presence of said marker being indicative of a pig more likely to have reproductive longevity potential; and

inferring that the pig is more likely to have reproductive longevity potential if the pig possesses said marker polymorphism.

Claim 26 (Currently amended): The method of claim 25 wherein the assaying step comprises amplifying the gene or a region thereof containing the marker polymorphism with a forward and a reverse sequence primer.

Claim 27 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:8 and the reverse primer is SEQ ID NO:9.

Claim 28 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:10 and the reverse primer is SEQ ID NO:11.

Claim 29 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:12 and said reverse primer is SEQ ID NO:13.

Claim 30 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:14 and the reverse primer is SEQ ID NO:15.

Claim 31 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:16 and the reverse primer is SEQ ID NO:17.

Claim 32 (Withdrawn): The method of claim 26 wherein the forward primer is SEQ ID NO:18 and the reverse primer is SEQ ID NO:19.

Claim 33 (Withdrawn): The method of claim 25 wherein the marker is DpnII.

Claim 34 (Withdrawn): The method of claim 25 wherein the marker is HpaII.

Claim 35 (Withdrawn): The method of claim 25 wherein the marker is TaqI.

Claim 36 (Withdrawn): The method of claim 25 wherein the marker is MnlI.

Claim 37 (Withdrawn): The method of claim 25 wherein the marker is AvaII.

Claim 38 (Withdrawn): The method of claim 33 wherein a G to A nucleotide substitution results in a restriction pattern characterized by a 328 nucleotide fragment, a 125 nucleotide fragment, and a 32 nucleotide fragment.

Claim 39 (Withdrawn): The method of claim 34 wherein an A to G nucleotide substitution results in a restriction pattern characterized by a 373 nucleotide fragment, a 134 nucleotide fragment, and a 127 nucleotide fragment.

Claim 40 (Withdrawn): The method of claim 34 wherein the deletion is characterized by a 12 bp fragment having SEQ ID NO:20 appearing once in the IGF-1R gene.

Claim 41 (Withdrawn): The method of claim 35 wherein a G to A nucleotide substitution results in a restriction pattern characterized by a 135 nucleotide fragment and an 84 nucleotide fragment.

Claim 42 (Withdrawn): The method of claim 36 wherein an G to C nucleotide substitution results in a restriction pattern characterized by a 137 nucleotide fragment, a 104 nucleotide fragment, a 55 nucleotide fragment, and an 11 nucleotide fragment.

Claim 43 (Withdrawn): The method of claim 37 wherein an G to A nucleotide substitution results in a restriction pattern characterized by a 122 nucleotide fragment, an 81 nucleotide fragment, a 60 nucleotide fragment, and a 44 nucleotide fragment.

Claim 44 (Canceled).

Claim 45 (Currently amended): A method for screening pigs to determine those more likely to exhibit favorable ~~traits associated with reproductive longevity potential~~ traits, said method comprising:

obtaining a genetic sample from a pig;

detecting the presence or absence of ~~at least one allele~~ a polymorphism in the IGF-1R gene corresponding to ~~at~~ position 3832 of SEQ ID NO:23, wherein the ~~presence of the allele~~ polymorphism is a thymidine at position 3832 of SEQ ID NO:23, the polymorphism is predictive of the pig having reproductive longevity potential, wherein the trait of reproductive longevity potential is characterized by an increase in the number of pregnancies or the duration of time a pig is capable of reproduction relative to the mean of a given population, group or species; and

inferring that the pig is more likely to exhibit favorable ~~traits associated with reproductive longevity~~ potential traits if the pig has a thymidine at position 3832.

Claim 46 (Withdrawn): The method of claim 45 wherein the allele is defined in intron 16 of the gene.

Claim 47 (Withdrawn): The method of claim 45 wherein the allele is defined in exon 21 at position 3876 of the gene.

Claim 48 (Withdrawn): The method of claim 45 wherein the allele is defined in exon 21 at positions 3896-3907 of the gene.

Claim 49 (Withdrawn): The method of claim 45 wherein the allele is defined at position 27 at the end of intron 16 of the gene.

Claim 50 (Withdrawn): The method of claim 45 wherein the allele is defined at position 73 at the end of intron 16 of the gene.

Claim 51 (Canceled).

Claim 52 (Withdrawn): A method for determining the haplotype of the IGF-1R gene of an animal comprising:
obtaining a genetic sample from an animal; and
analyzing the genetic sample for the presence of an IGF-1R gene A1D1, A1D2, or A2D1
haplotype allele, wherein the haplotype effects reproductive performance or the ability to sustain stress factors.

Claim 53 (Withdrawn): The method of claim 52 wherein the A1D1 allele is indicative of having a favorable effect on lactation and pregnancy stress.

Claim 54 (Withdrawn): The method of claim 52 wherein the A1D2 allele is indicative of having a negative effect on reproductive performance.

Claim 55 (Withdrawn): The method of claim 52 wherein the A2D1 allele is indicative of reproductive longevity.

Claim 56 (Withdrawn): The method of claim 52 wherein the animal is a mouse.

Claims 57-64 (Cancelled).

Claim 65 (Withdrawn): A method for genetically identifying an animal comprising: obtaining a sample of genetic material from an animal; and assaying for the presence of a genotype in the IGF-1R gene sequence as set forth in SEQ ID NO:1 or a region thereof in the sample, wherein the animal possesses a nucleic acid sequence having at least 95% sequence identity to SEQ ID NO:1 or a fragment thereof.

Claim 66 (Withdrawn): The method of claim 65 wherein the polymorphism is identified by a G to A nucleotide substitution in intron 16.

Claim 67 (Withdrawn): The method of claim 65 wherein the polymorphism is identified by an A to G nucleotide substitution in exon 21.

Claim 68 (Withdrawn): The method of claim 65 wherein the polymorphism is identified as a 12 bp deletion in exon 21.

Claim 69 (Withdrawn): The method of claim 65 wherein the polymorphism is identified as an insertion of a G nucleotide in intron 16 at position 176.

Claim 70 (Withdrawn): The method of claim 65 wherein the animal is a mouse.

Claim 71 (Canceled).

Claim 72 (Withdrawn): The method of claim 71 wherein said polymorphism is identified as a G to A nucleotide substitution in intron 16.

Claim 73 (Withdrawn): The method of claim 71 wherein said polymorphism is identified as a G to C nucleotide substitution in intron 16.

Claim 74 (Withdrawn): The method of claim 71 wherein said polymorphism is identified as a G to A nucleotide substitution in exon 8.

Claim 75 (Canceled).

Claim 76 (Withdrawn): The method of claim 65 wherein the polymorphism is an A to G nucleotide substitution in exon 21 at position 3876.

Claim 77 (Withdrawn): The method of claim 65 wherein the polymorphism is a 12 bp deletion in exon 21 at positions 3896-3907.

Claim 78 (Withdrawn): The method of claim 71 wherein said polymorphism is a G to A nucleotide substitution at position 27 from the end of intron 16.

Claim 79 (Withdrawn): The method of claim 71 wherein said polymorphism is a G to C nucleotide substitution at position 73 from the end of intron 16.

Claim 80 (Withdrawn): A method for genetically identifying cattle with respect to its potential to reproductive longevity comprising:
obtaining a sample of genetic material from a cow; and

assaying for the presence of a polymorphism in the insulin-like growth factor 1 receptor gene (IGF-1R), wherein the polymorphism is associated with reproductive longevity.

Claim 81 (New): A method of genetically typing pigs to determine those with favorable reproductive longevity potential traits, comprising:
obtaining a sample of genetic material from said pig; and
assaying for the presence of a genotype in said pig which is associated with reproductive longevity potential, said genotype characterized by the following: a polymorphism in the IGF-1R gene corresponding to position 3832 of SEQ ID NO:23, wherein the polymorphism is a thymidine at position 3832 of SEQ ID NO:23, said polymorphism being associated with reproductive longevity potential, wherein the trait of reproductive longevity potential is characterized by an increase in the number of pregnancies or the duration of time a pig is capable of reproduction relative to the mean of a given population, group or species.